

SEQUENCE.TXT
SEQUENCE LISTING

IAP8 Rec'd PCT/PID 08 DEC 2005

<110> Tours Nestlé Research Center

<120> Implication Of Proteinase And Proteinase Inhibitor In Coffee Flavour

<130> Patent Proteinase and Proteinase Inhibitor Coffee

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 1543

<212> DNA

<213> Coffea canephora

<220>

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<222> (1)..(1543)

<223>

<220>

<221> CDS

<222> (122)..(1315)

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g atg atg atg aca agc gga ggt ctg atg cta acc tgc act ctg gct att	169
Met Met Met Thr Ser Gly Gly Leu Met Leu Thr Cys Thr Leu Ala Ile	
1 5 10 15	

SEQUENCE.TXT

acc ctc tta tcc tgc gca ctc atc tct tca acc act ttc caa cat gaa Thr Leu Leu Ser Cys Ala Leu Ile Ser Ser Thr Thr Phe Gln His Glu 20 25 30	217
att cag tat cga gta caa gac ccg tta atg ata cgc caa gtc acc gac Ile Gln Tyr Arg Val Gln Asp Pro Leu Met Ile Arg Gln Val Thr Asp 35 40 45	265
aat cac cac cac cgc cac ccc ggt agg tct tct gca aac cat cgt Asn His His His Arg His His Pro Gly Arg Ser Ser Ala Asn His Arg 50 55 60	313
cta ctg ggc acc acc aca gag gtt cac ttc aag tcc ttc gtg gag gag Leu Leu Gly Thr Thr Glu Val His Phe Lys Ser Phe Val Glu Glu 65 70 75 80	361
tac gag aaa act tac tct acg cac gag gag tac gtg cac cgc ctg ggg Tyr Glu Lys Thr Tyr Ser Thr His Glu Glu Tyr Val His Arg Leu Gly 85 90 95	409
att ttc gcc aag aac ctc atc aag gcc gcg gag cac cag gcc atg gac Ile Phe Ala Lys Asn Leu Ile Lys Ala Ala Glu His Gln Ala Met Asp 100 105 110	457
ccc tcc gca atc cac ggc gtc acc cag ttc tct gat ctc acc gag gag Pro Ser Ala Ile His Gly Val Thr Gln Phe Ser Asp Leu Thr Glu Glu 115 120 125	505
gag ttt gag gct acg tac atg ggc ctt aaa ggt ggc gct gga gtt ggt Glu Phe Glu Ala Thr Tyr Met Gly Leu Lys Gly Gly Ala Gly Val Gly 130 135 140	553
ggg acc acc cag ctg ggg aaa gat gat ggg gat gag agt gca gca gag Gly Thr Thr Gln Leu Gly Lys Asp Asp Gly Asp Glu Ser Ala Ala Glu 145 150 155 160	601
gtg atg atg gat gta tct gat ttg ccg gag agt ttt gat tgg aga gaa Val Met Met Asp Val Ser Asp Leu Pro Glu Ser Phe Asp Trp Arg Glu 165 170 175	649
aaa ggt gct gtg acc gaa gtg aag acg cag gga aga tgt gga tcg tgt Lys Gly Ala Val Thr Glu Val Lys Thr Gln Gly Arg Cys Gly Ser Cys 180 185 190	697
tgg gct ttt agt aca act gga gct att gaa gga gct aat ttc att gca Trp Ala Phe Ser Thr Thr Gly Ala Ile Glu Gly Ala Asn Phe Ile Ala 195 200 205	745
act ggc aag ctt ctc agc cta agt gaa cag cag ctt gtg gat tgt gat Thr Gly Lys Leu Leu Ser Leu Ser Glu Gln Gln Leu Val Asp Cys Asp 210 215 220	793
cat atg tgt gat tta aaa gaa aaa gat gac tgt gat gat gga tgc tcc His Met Cys Asp Leu Lys Glu Lys Asp Asp Cys Asp Asp Gly Cys Ser 225 230 235 240	841
gga ggg cta atg aca act gct ttc aac tac ttg ata gag gca gga ggt Gly Gly Leu Met Thr Thr Ala Phe Asn Tyr Leu Ile Glu Ala Gly Gly 245 250 255	889
ata gag gag gag gta acc tat ccc tac act ggg aaa cgc gga gaa tgc Ile Glu Glu Glu Val Thr Tyr Pro Tyr Thr Gly Lys Arg Gly Glu Cys 260 265 270	937

SEQUENCE.TXT

aaa ttc aat cct gag aaa gtt gcg gtg aaa gtg cg ^g aat ttc gca aaa Lys Phe Asn Pro Glu Lys Val Ala Val Lys Val Arg Asn Phe Ala Lys 275 280 285	985
atc cct gag gat gag agt caa att gct gcc aat gta gtg cat aat ggc Ile Pro Glu Asp Glu Ser Gln Ile Ala Ala Asn Val Val His Asn Gly 290 295 300	1033
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ggt gtg tca tgt cct ctt att tgt gac aaa aag agg atc aac cat ggt Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly 325 330 335	1129
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ggc tac aag cca tac tgg att atc aag aac tca tgg ggg aag cgt tgg Gly Tyr Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Lys Arg Trp 355 360 365	1225
ggc gaa cat ggt tgc tac cgg ctt tgt cga ggg cac aac atg tgt gga Gly Glu His Gly Cys Tyr Arg Leu Cys Arg Gly His Asn Met Cys Gly 370 375 380	1273
atg agc aca atg gtt tca gct gtg gtg aca cag acc tct tga Met Ser Thr Met Val Ser Ala Val Val Thr Gln Thr Ser 385 390 395	1315
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<210> 2

<211> 397

<212> PRT

<213> Coffea canephora

<400> 2

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Ile Gln Tyr Arg Val Gln Asp Pro Leu Met Ile Arg Gln Val Thr Asp

35 40 45
SEQUENCE.TXT

Asn His His His Arg His His Pro Gly Arg Ser Ser Ala Asn His Arg
50 55 60

Leu Leu Gly Thr Thr Thr Glu Val His Phe Lys Ser Phe Val Glu Glu
65 70 75 80

Tyr Glu Lys Thr Tyr Ser Thr His Glu Glu Tyr Val His Arg Leu Gly
85 90 95

Ile Phe Ala Lys Asn Leu Ile Lys Ala Ala Glu His Gln Ala Met Asp
100 105 110

Pro Ser Ala Ile His Gly Val Thr Gln Phe Ser Asp Leu Thr Glu Glu
115 120 125

Glu Phe Glu Ala Thr Tyr Met Gly Leu Lys Gly Gly Ala Gly Val Gly
130 135 140

Gly Thr Thr Gln Leu Gly Lys Asp Asp Gly Asp Glu Ser Ala Ala Glu
145 150 155 160

Val Met Met Asp Val Ser Asp Leu Pro Glu Ser Phe Asp Trp Arg Glu
165 170 175

Lys Gly Ala Val Thr Glu Val Lys Thr Gln Gly Arg Cys Gly Ser Cys
180 185 190

Trp Ala Phe Ser Thr Thr Gly Ala Ile Glu Gly Ala Asn Phe Ile Ala
195 200 205

Thr Gly Lys Leu Leu Ser Leu Ser Glu Gln Gln Leu Val Asp Cys Asp
210 215 220

His Met Cys Asp Leu Lys Glu Lys Asp Asp Cys Asp Asp Gly Cys Ser
225 230 235 240

Gly Gly Leu Met Thr Thr Ala Phe Asn Tyr Leu Ile Glu Ala Gly Gly
245 250 255

Ile Glu Glu Glu Val Thr Tyr Pro Tyr Thr Gly Lys Arg Gly Glu Cys
260 265 270

Lys Phe Asn Pro Glu Lys Val Ala Val Lys Val Arg Asn Phe Ala Lys
275 280 285

SEQUENCE.TXT

Ile Pro Glu Asp Glu Ser Gln Ile Ala Ala Asn Val Val His Asn Gly
290 295 300

Pro Leu Ala Ile Gly Leu Asn Ala Val Phe Met Gln Thr Tyr Ile Gly
305 310 315 320

Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly
325 330 335

Val Leu Leu Val Gly Tyr Gly Ser Arg Gly Phe Ser Ile Leu Arg Leu
340 345 350

Gly Tyr Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Lys Arg Trp
355 360 365

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370 375 380

Met Ser Thr Met Val Ser Ala Val Val Thr Gln Thr Ser
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<212> DNA

<213> Coffea canephora

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<222> (1)..(726)

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<221> CDS

<222> (79)..(498)

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Met Ala Lys Pro Ser Ser Ser Leu Leu Thr Leu

-60

111

6/23

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ctc caa gtt aat gcc ttg gga agg aaa gtg gga gca agg gag aag att Leu Gln Val Asn Ala Leu Gly Arg Lys Val Gly Ala Arg Glu Lys Ile 30 35 40			207
gag gat gtg aag agc aac aaa gaa gtt caa gaa ctt ggg gaa tat tgt Glu Asp Val Lys Ser Asn Lys Glu Val Gln Glu Leu Gly Glu Tyr Cys 45 50 55			255
gtt tct gag tac aac aag agt ttg cgg aag aag aac aac gaa agt ggt Val Ser Glu Tyr Asn Lys Ser Leu Arg Lys Lys Asn Asn Glu Ser Gly 60 65 70 75			303
gct cct ata atc ttc aca tct gtg gtg gag gct gag aag cag gtg gtt Ala Pro Ile Ile Phe Thr Ser Val Val Glu Ala Glu Lys Gln Val Val 80 85 90			351
gct ggg atc aaa tat tat ctc aag att aag gcc acc act tct tct ggg Ala Gly Ile Lys Tyr Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly 95 100 105			399
gtt ccc aag gtt tac gat gcc att gtg gtg gtt cgg cct tgg gtt cat Val Pro Lys Val Tyr Asp Ala Ile Val Val Val Arg Pro Trp Val His 110 115 120			447
act aag cca agg cag ttg ctc aac ttc tcc cct tcc cct gcc act aaa Thr Lys Pro Arg Gln Leu Leu Asn Phe Ser Pro Ser Pro Ala Thr Lys 125 130 135			495
tga agaagaaaat gttggaaaaat ttggaaactgt ttggggagatc taatctgatg attatttagta ctttcagtg caaattctct ttgctgttaa gtgttcggtt tttttttttt ccctgtgtct atttatgacc gtggtcatga tgatatggtg tatgatccag taataattaa aatctgttgc ataaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa			548 608 668 726
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SEQUENCE.TXT

Leu Gly Arg Lys Val Gly Ala Arg Glu Lys Ile Glu Asp Val Lys Ser
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Asn Lys Glu Val Gln Glu Leu Gly Glu Tyr Cys Val Ser Glu Tyr Asn
50 55 60

Lys Ser Leu Arg Lys Lys Asn Asn Glu Ser Gly Ala Pro Ile Ile Phe
65 70 75 80

Thr Ser Val Val Glu Ala Glu Lys Gln Val Val Ala Gly Ile Lys Tyr
85 90 95

Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly Val Pro Lys Val Tyr
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Asp Ala Ile Val Val Val Arg Pro Trp Val His Thr Lys Pro Arg Gln
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Leu Leu Asn Phe Ser Pro Ser Pro Ala Thr Lys
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<222> (1)..(2282)

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<222> (439)..(1731)

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tgttattttt gatgtagaag gtaacaataa tgtggttttt gaggtgaaac ataaatttaa	300
agggagaagg aatgagaatg gaggaaaggagg gtcttttga cttcactcaa ggctcatgat	360
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aat ggt tcc cct aca gat gca gcg ctc tat ttc act aag ctt tcg att Asn Gly Ser Pro Thr Asp Ala Ala Leu Tyr Phe Thr Lys Leu Ser Ile 15 20 25	519
ggg act cct cct cag gat tat tat gtg caa gtg gat aca gga agt gac Gly Thr Pro Pro Gln Asp Tyr Tyr Val Gln Val Asp Thr Gly Ser Asp 30 35 40	567
att ctc tgg gta aac tgg tct ggt tgg ttc aga tgg ccc aag aaa agc Ile Leu Trp Val Asn Cys Ala Gly Cys Val Arg Cys Pro Lys Lys Ser 45 50 55	615
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ggg aga ctt gtt act tgg gat caa gac ttt tgc ttg tct gca ttc aat Gly Arg Leu Val Thr Cys Asp Gln Asp Phe Cys Leu Ser Ala Phe Asn 80 85 90	711
gcc cca gcc tct gat tgc aag gtt ggt aac ccc tgg tct gca tat tct gtt Ala Pro Ala Ser Asp Cys Lys Val Gly Asn Pro Cys Ala Tyr Ser Val 95 100 105	759
act tac gga gac ggg agc tca acc ggc gga tat ttt gtc aga gac tat Thr Tyr Gly Asp Gly Ser Ser Thr Gly Gly Tyr Phe Val Arg Asp Tyr 110 115 120	807
gca aaa ctt aat caa ctg acg gga aat ctt caa acc ata ccc atg aat Ala Lys Leu Asn Gln Leu Thr Gly Asn Leu Gln Thr Ile Pro Met Asn 125 130 135	855
ggt agt ata gtg ttt ggg tgg tct tca tct caa caa tct gga gag cta ggg Gly Ser Ile Val Phe Gly Cys Ser Ser Gln Gln Ser Gly Glu Leu Gly 140 145 150 155	903
tca tct act gaa gca gtt gat ggc ata att ggt ttt gga caa gca aat Ser Ser Thr Glu Ala Val Asp Gly Ile Ile Gly Phe Gly Gln Ala Asn 160 165 170	951
tca tct att att tca cag ctt gct tca gca gga aag gtt aaa aaa ata Ser Ser Ile Ile Ser Gln Leu Ala Ser Ala Gly Lys Val Lys Lys Ile 175 180 185	999
ttt tca cat tgc ttg gat ggt atc aat gga gga ggc ata ttt gct att Phe Ser His Cys Leu Asp Gly Ile Asn Gly Gly Ile Phe Ala Ile 190 195 200	1047
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Gly Gln Val Val Gln Pro Lys Leu Lys Thr Thr Pro Leu Val Pro Asn	
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Glu Ala His Tyr Asn Val Val Leu Asn Ala Ile Glu Val Gly Gly Asp	
220 225 230 235	
gtt cta aac ctt ccc tca gat gta tta gga ggt gga tct gga agt ggt	1191
Val Leu Asn Leu Pro Ser Asp Val Leu Gly Gly Ser Gly Ser Gly	
240 245 250	
aca ata ata gac agt ggt aca acc ttg gct tat ctt cct gat gat gtc	1239
Thr Ile Ile Asp Ser Gly Thr Thr Leu Ala Tyr Leu Pro Asp Asp Val	
255 260 265	
tat act cca ctt atg gaa aag att acg gca tcc caa tcc aac ttg aaa	1287
Tyr Thr Pro Leu Met Glu Lys Ile Thr Ala Ser Gln Ser Asn Leu Lys	
270 275 280	
atc cat att gtt gaa aat cag ttc aag tgc ttt gtc tat agt gga aat	1335
Ile His Ile Val Glu Asn Gln Phe Lys Cys Phe Val Tyr Ser Gly Asn	
285 290 295	
gtt gat gat gga ttt cca gtt gta tct ttc cac ttt gag gat tca ctt	1383
Val Asp Asp Gly Phe Pro Val Val Ser Phe His Phe Glu Asp Ser Leu	
300 305 310 315	
tct ttg aca gtt tat ccc cat gaa tat ctc ttt gat ctt cat gat gat	1431
Ser Leu Thr Val Tyr Pro His Glu Tyr Leu Phe Asp Leu His Asp Asp	
320 325 330	
caa tgg tgt att ggt tgg cag aat aag ggt atg cag aca aga gat gga	1479
Gln Trp Cys Ile Gly Trp Gln Asn Lys Gly Met Gln Thr Arg Asp Gly	
335 340 345	
agg gaa gta act ctt ttg gga gat ctt gta ctc gca aac aag ctt gtt	1527
Arg Glu Val Thr Leu Leu Gly Asp Leu Val Leu Ala Asn Lys Leu Val	
350 355 360	
tcg tat gat ctt gaa aat caa acc att gga tgg gct gaa tat aat tgc	1575
Ser Tyr Asp Leu Glu Asn Gln Thr Ile Gly Trp Ala Glu Tyr Asn Cys	
365 370 375	
tct tcg agc atc aaa ttg aga gac gag aag tca gga aac gtg tat gct	1623
Ser Ser Ser Ile Lys Leu Arg Asp Glu Lys Ser Gly Asn Val Tyr Ala	
380 385 390 395	
gtg ggc tct cat atc att tct tca gct cgc ggc ctg aat gct gga aag	1671
Val Gly Ser His Ile Ile Ser Ser Ala Arg Gly Leu Asn Ala Gly Lys	
400 405 410	
gct cta agg ttc cta ttg tta atc atc aca tca ttg ttg cat gca ctt	1719
Ala Leu Arg Phe Leu Leu Ile Ile Thr Ser Leu Leu His Ala Leu	
415 420 425	
ttg atc cca tga acatTTaaaaa tcatactagc tgagaaggag gcattatgtat	1771
Leu Ile Pro	
430	
agcgtaaccat ggtactcata gtgatcaggc atcttgctga ttctttggac cattataatt	1831
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SEQUENCE.TXT

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tgatacccca	gatgattaag	gaaagcctat	aggaaacaga	tggtgggaag	gagtatacat	2071
tctttctgac	tctttggAAC	ttccttagcgt	atacacatat	ttcacacgga	atgtatctta	2131
taattcatct	gttctttctg	tttattgtca	acttgttca	aatgattgga	gtagctgcaa	2191
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<212> PRT

<213> Coffea canephora

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				20				25				30			

Asp	Tyr	Tyr	Val	Gln	Val	Asp	Thr	Gly	Ser	Asp	Ile	Leu	Trp	Val	Asn
35						40					45				

Cys	Ala	Gly	Cys	Val	Arg	Cys	Pro	Lys	Lys	Ser	Ser	Leu	Gly	Ile	Asp
50						55				60					

Leu	Thr	Leu	Tyr	Asp	Met	Lys	Ala	Ser	Ser	Thr	Gly	Arg	Leu	Val	Thr
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Cys	Asp	Gln	Asp	Phe	Cys	Leu	Ser	Ala	Phe	Asn	Ala	Pro	Ala	Ser	Asp
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Cys	Lys	Val	Gly	Asn	Pro	Cys	Ala	Tyr	Ser	Val	Thr	Tyr	Gly	Asp	Gly
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Ser	Ser	Thr	Gly	Gly	Tyr	Phe	Val	Arg	Asp	Tyr	Ala	Lys	Leu	Asn	Gln
115					120						125				

Leu	Thr	Gly	Asn	Leu	Gln	Thr	Ile	Pro	Met	Asn	Gly	Ser	Ile	Val	Phe
130					135					140					

SEQUENCE.TXT

Gly Cys Ser Ser Gln Gln Ser Gly Glu Leu Gly Ser Ser Thr Glu Ala
145 150 155 160

Val Asp Gly Ile Ile Gly Phe Gly Gln Ala Asn Ser Ser Ile Ile Ser
165 170 175

Gln Leu Ala Ser Ala Gly Lys Val Lys Lys Ile Phe Ser His Cys Leu
180 185 190

Asp Gly Ile Asn Gly Gly Ile Phe Ala Ile Gly Gln Val Val Gln
195 200 205

Pro Lys Leu Lys Thr Thr Pro Leu Val Pro Asn Glu Ala His Tyr Asn
210 215 220

Val Val Leu Asn Ala Ile Glu Val Gly Gly Asp Val Leu Asn Leu Pro
225 230 235 240

Ser Asp Val Leu Gly Gly Ser Gly Ser Gly Thr Ile Ile Asp Ser
245 250 255

Gly Thr Thr Leu Ala Tyr Leu Pro Asp Asp Val Tyr Thr Pro Leu Met
260 265 270

Glu Lys Ile Thr Ala Ser Gln Ser Asn Leu Lys Ile His Ile Val Glu
275 280 285

Asn Gln Phe Lys Cys Phe Val Tyr Ser Gly Asn Val Asp Asp Gly Phe
290 295 300

Pro Val Val Ser Phe His Phe Glu Asp Ser Leu Ser Leu Thr Val Tyr
305 310 315 320

Pro His Glu Tyr Leu Phe Asp Leu His Asp Asp Gln Trp Cys Ile Gly
325 330 335

Trp Gln Asn Lys Gly Met Gln Thr Arg Asp Gly Arg Glu Val Thr Leu
340 345 350

Leu Gly Asp Leu Val Leu Ala Asn Lys Leu Val Ser Tyr Asp Leu Glu
355 360 365

Asn Gln Thr Ile Gly Trp Ala Glu Tyr Asn Cys Ser Ser Ser Ile Lys
370 375 380

Leu Arg Asp Glu Lys Ser Gly Asn Val Tyr Ala Val Gly Ser His Ile
385 390 395 400

12/23

SEQUENCE.TXT

Ile Ser Ser Ala Arg Gly Leu Asn Ala Gly Lys Ala Leu Arg Phe Leu
 405 410 415

Leu Leu Ile Ile Thr Ser Leu Leu His Ala Leu Leu Ile Pro
 420 425 430

<210> 7

<211> 1819

<212> DNA

<213> Coffea canephora

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<222> (1)..(1732)

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<222> (79)..(1602)

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 Met Glu Arg Arg Tyr Leu Trp Ala Ala Phe Val
 1 5 10

tta ggg gcg att gtg tgt tct cta ttt cct ctt cct tct gaa gga tta 159
 Leu Gly Ala Ile Val Cys Ser Leu Phe Pro Leu Pro Ser Glu Gly Leu
 15 20 25

aag cga att agc ctg aaa aaa aaa ccc tta gat att caa agc ata aga 207
 Lys Arg Ile Ser Leu Lys Lys Pro Leu Asp Ile Gln Ser Ile Arg
 30 35 40

gct gcc aaa tta gct cat ctg gag agc aca cat ggc gct ggt agg aaa 255
 Ala Ala Lys Leu Ala His Leu Glu Ser Thr His Gly Ala Gly Arg Lys
 45 50 55

gag atg gac aac aat tta ggc agt tcc aat gag gac ata ttg cct tta 303
 Glu Met Asp Asn Asn Leu Gly Ser Ser Asn Glu Asp Ile Leu Pro Leu
 60 65 70 75

aag aat tac ctg gat gcc cag tac tat gga gag att gga att ggt act 351

SEQUENCE.TXT

Lys Asn Tyr Leu Asp Ala Gln Tyr Tyr	Gly Glu Ile Gly Ile Gly Thr		
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Pro Pro Gln Lys Phe Thr Val Ile Phe Asp Thr Gly Ser Ser Asn Leu			
95	100	105	
tgg gtg cca tcg gca aaa tgt tac ttc tct att gcc tgc tgg ctc cac		447	
Trp Val Pro Ser Ala Lys Cys Tyr Phe Ser Ile Ala Cys Trp Leu His			
110	115	120	
tcc aag tac aag gca aag aag tca agt act tat aca gcc ata ggg aaa		495	
Ser Lys Tyr Lys Ala Lys Ser Ser Thr Tyr Thr Ala Ile Gly Lys			
125	130	135	
tct tgt tca att cgt tat ggt tct gga tca att tct gga ttc tcc agt		543	
Ser Cys Ser Ile Arg Tyr Gly Ser Gly Ser Ile Ser Gly Phe Ser Ser			
140	145	150	155
cag gat aac gtt gaa gtt ggt gat ctt gtt gtc aaa gat caa gtt ttt		591	
Gln Asp Asn Val Glu Val Gly Asp Leu Val Val Lys Asp Gln Val Phe			
160	165	170	
att gaa gct tca cga gaa gga agt ctt aca ttt gta att gcc aag ttt		639	
Ile Glu Ala Ser Arg Glu Gly Ser Leu Thr Phe Val Ile Ala Lys Phe			
175	180	185	
gac ggg ata ctt ggc ctt gga ttc cag gag atc gct gtt gat aac atg		687	
Asp Gly Ile Leu Gly Leu Gly Phe Gln Glu Ile Ala Val Asp Asn Met			
190	195	200	
gtg ccg gtc tgg tat aat atg gtc gac caa ggt ctc gtg gat gag caa		735	
Val Pro Val Trp Tyr Asn Met Val Asp Gln Gly Leu Val Asp Glu Gln			
205	210	215	
gta ttc tct ttc tgg ctt aac cgc gac cca aat gct gaa gac gga ggt		783	
Val Phe Ser Phe Trp Leu Asn Arg Asp Pro Asn Ala Glu Asp Gly Gly			
220	225	230	235
gag ctg gtc ttt ggt ggt gta gat aca aat cac ttc aag gga aag cat		831	
Glu Leu Val Phe Gly Gly Val Asp Thr Asn His Phe Lys Gly Lys His			
240	245	250	
aca tat gtt cct gta act cag aag gga tac tgg caa ttt aaa atg gga		879	
Thr Tyr Val Pro Val Thr Gln Lys Gly Tyr Trp Gln Phe Lys Met Gly			
255	260	265	
gat ttt ctc att ggg aac gtc tca aca ggc ttt tgt gaa gga ggt tgt		927	
Asp Phe Leu Ile Gly Asn Val Ser Thr Gly Phe Cys Glu Gly Gly Cys			
270	275	280	
gct gct att gtg gac tct gga aca tcg ttg ctc gct ggt cca act act		975	
Ala Ala Ile Val Asp Ser Gly Thr Ser Leu Leu Ala Gly Pro Thr Thr			
285	290	295	
gtt gtg act caa att aat cat gcc att gga gct gaa gga gta gtt agc		1023	
Val Val Thr Gln Ile Asn His Ala Ile Gly Ala Glu Gly Val Val Ser			
300	305	310	315
act gaa tgt aaa gaa att gtt tca cag tat ggt gaa ctg att tgg gat		1071	
Thr Glu Cys Lys Glu Ile Val Ser Gln Tyr Gly Glu Leu Ile Trp Asp			
320	325	330	

SEQUENCE.TXT

ctc ctc gta tca ggg gta cta ccc gac aga gtt tgt aaa caa gct ggt Leu Leu Val Ser Gly Val Leu Pro Asp Arg Val Cys Lys Gln Ala Gly 335 340 345	1119
tta tgt ccc ctt cgt ggt gct cag cat gag aat gct tat atc aag tca Leu Cys Pro Leu Arg Gly Ala Gln His Glu Asn Ala Tyr Ile Lys Ser 350 355 360	1167
gtc gtc gac gag gag aac aag gag gaa gct tct gtt ggt gaa tcc ccg Val Val Asp Glu Glu Asn Lys Glu Glu Ala Ser Val Gly Glu Ser Pro 365 370 375	1215
atg tgt act gct tgt gaa atg gct gtt tgg atg caa aac cag ctg Met Cys Thr Ala Cys Glu Met Ala Val Val Trp Met Gln Asn Gln Leu 380 385 390 395	1263
aaa cag cag gga act aag gag aaa gtg ctt gca tat gtg aat cag ctt Lys Gln Gln Gly Thr Lys Glu Lys Val Leu Ala Tyr Val Asn Gln Leu 400 405 410	1311
tgt gaa agc ata cca agt ccc atg gga gaa tcc atc att gac tgc aac Cys Glu Ser Ile Pro Ser Pro Met Gly Glu Ser Ile Ile Asp Cys Asn 415 420 425	1359
agt tta tcc acc ctg cca aat gtt tca ttc acc atc gga ggg aaa agt Ser Leu Ser Thr Leu Pro Asn Val Ser Phe Thr Ile Gly Gly Lys Ser 430 435 440	1407
ttt gag ctg acc ctt aag gag tat gtt ctt cga act gga gaa ggc ttt Phe Glu Leu Thr Leu Lys Glu Tyr Val Leu Arg Thr Gly Glu Gly Phe 445 450 455	1455
gct gaa gtc tgc atc agt gga ttc atg gct atg gat gtg ccg ccg cct Ala Glu Val Cys Ile Ser Gly Phe Met Ala Met Asp Val Pro Pro Pro 460 465 470 475	1503
cgt ggt ccc atc tgg gtt ctg gga gat gtg ttc atg gga gtg tac cac Arg Gly Pro Ile Trp Val Leu Gly Asp Val Phe Met Gly Val Tyr His 480 485 490	1551
acc gtg ttt gat tat ggt aat ctc cggt atg ggt ttc gca aga gct gct Thr Val Phe Asp Tyr Gly Asn Leu Arg Met Gly Phe Ala Arg Ala Ala 495 500 505	1599
tag acaagactgt ttatttcgtc tactgtttga cggccctaag agaagctatg	1652
aagacatgt atagcttgta aatttagatt taatttatgct tggctggttt atgggtggtg	1712
cttttaatat tatatgtaat gtaagcagat atgttacctt gtttagagt ttcaaggaaa	1772
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<210> 8

<211> 507

<212> PRT

<213> Coffea canephora

SEQUENCE.TXT

<400> 8

Met Glu Arg Arg Tyr Leu Trp Ala Ala Phe Val Leu Gly Ala Ile Val
1 5 10 15

Cys Ser Leu Phe Pro Leu Pro Ser Glu Gly Leu Lys Arg Ile Ser Leu
20 25 30

Lys Lys Lys Pro Leu Asp Ile Gln Ser Ile Arg Ala Ala Lys Leu Ala
35 40 45

His Leu Glu Ser Thr His Gly Ala Gly Arg Lys Glu Met Asp Asn Asn
50 55 60

Leu Gly Ser Ser Asn Glu Asp Ile Leu Pro Leu Lys Asn Tyr Leu Asp
65 70 75 80

Ala Gln Tyr Tyr Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Lys Phe
85 90 95

Thr Val Ile Phe Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Ala
100 105 110

Lys Cys Tyr Phe Ser Ile Ala Cys Trp Leu His Ser Lys Tyr Lys Ala
115 120 125

Lys Lys Ser Ser Thr Tyr Thr Ala Ile Gly Lys Ser Cys Ser Ile Arg
130 135 140

Tyr Gly Ser Gly Ser Ile Ser Gly Phe Ser Ser Gln Asp Asn Val Glu
145 150 155 160

Val Gly Asp Leu Val Val Lys Asp Gln Val Phe Ile Glu Ala Ser Arg
165 170 175

Glu Gly Ser Leu Thr Phe Val Ile Ala Lys Phe Asp Gly Ile Leu Gly
180 185 190

Leu Gly Phe Gln Glu Ile Ala Val Asp Asn Met Val Pro Val Trp Tyr
195 200 205

Asn Met Val Asp Gln Gly Leu Val Asp Glu Gln Val Phe Ser Phe Trp
210 215 220

Leu Asn Arg Asp Pro Asn Ala Glu Asp Gly Gly Glu Leu Val Phe Gly
225 230 235 240

Gly Val Asp Thr Asn His Phe Lys Gly Lys His Thr Tyr Val Pro Val

SEQUENCE.TXT

245	250	255
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Thr Gln Lys Gly Tyr Trp Gln Phe Lys Met Gly Asp Phe Leu Ile Gly
260 265 270

Asn Val Ser Thr Gly Phe Cys Glu Gly Gly Cys Ala Ala Ile Val Asp
275 280 285

Ser Gly Thr Ser Leu Leu Ala Gly Pro Thr Thr Val Val Thr Gln Ile
290 295 300

Asn His Ala Ile Gly Ala Glu Gly Val Val Ser Thr Glu Cys Lys Glu
305 310 315 320

Ile Val Ser Gln Tyr Gly Glu Leu Ile Trp Asp Leu Leu Val Ser Gly
325 330 335

Val Leu Pro Asp Arg Val Cys Lys Gln Ala Gly Leu Cys Pro Leu Arg
340 345 350

Gly Ala Gln His Glu Asn Ala Tyr Ile Lys Ser Val Val Asp Glu Glu
355 360 365

Asn Lys Glu Glu Ala Ser Val Gly Glu Ser Pro Met Cys Thr Ala Cys
370 375 380

Glu Met Ala Val Val Trp Met Gln Asn Gln Leu Lys Gln Gln Gly Thr
385 390 395 400

Lys Glu Lys Val Leu Ala Tyr Val Asn Gln Leu Cys Glu Ser Ile Pro
405 410 415

Ser Pro Met Gly Glu Ser Ile Ile Asp Cys Asn Ser Leu Ser Thr Leu
420 425 430

Pro Asn Val Ser Phe Thr Ile Gly Gly Lys Ser Phe Glu Leu Thr Leu
435 440 445

Lys Glu Tyr Val Leu Arg Thr Gly Glu Gly Phe Ala Glu Val Cys Ile
450 455 460

Ser Gly Phe Met Ala Met Asp Val Pro Pro Pro Arg Gly Pro Ile Trp
465 470 475 480

Val Leu Gly Asp Val Phe Met Gly Val Tyr His Thr Val Phe Asp Tyr
485 490 495

SEQUENCE.TXT

Gly Asn Leu Arg Met Gly Phe Ala Arg Ala Ala
500 505

<210> 9
<211> 726
<212> DNA
<213> Coffea canephora

<400> 9
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cagtgaatct aagggaatg agaacagcct tgaaattgag agcctggcta agtttgctgt 180
ggatgattac aacaagaaac agaatgccct tttggaattt cagaaggta tcaacagtaa 240
agagcaggtt gttgctggta ccgtgtacta tctgaccatt gaggtgaaag atgggaatga 300
gaagaagctt tatgaggcca aagtttgggt gaagccatgg ttgaacttca aggaggttca 360
agaattcaag cctgctgctg gtgatactag tgcctaaatt tgcttcttaa caatgcgcta 420
ttgccttattt gccttaga aataaaagcta acgcgtaaat gtctttcagt tggaaagatt 480
ggagttcaa acatgcttag tttgtatatg ctataactcg taatattaac atgttagtaa 540
catgttatct tatgttggat agatgttaag accaacataa tcttcgctga tgttcggttc 600
gatgtgatct gatcctgtgg tttttataacc actctggctt gagtacattt acccttagtc 660
cctttatgtg gctttattt ttgaaataaa aagtcatttt tctcttaaaa aaaaaaaaaa 720
aaaaaaaaa 726

<210> 10
<211> 98
<212> PRT
<213> Coffea canephora

<400> 10
Met Ala Lys Val Gly Gly Ile Ser Glu Ser Lys Gly Asn Glu Asn Ser 10 15
1 5

Leu Glu Ile Glu Ser Leu Ala Lys Phe Ala Val Asp Asp Tyr Asn Lys 20 25 30

Lys Gln Asn Ala Leu Leu Glu Phe Gln Lys Val Ile Asn Ser Lys Glu

SEQUENCE.TXT

35

40

45

Gln Val Val Ala Gly Thr Val Tyr Tyr Leu Thr Ile Glu Val Lys Asp
50 55 60

Gly Asn Glu Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp
65 70 75 80

Leu Asn Phe Lys Glu Val Gln Glu Phe Lys Pro Ala Ala Gly Asp Thr
85 90 95

Ser Ala

<210> 11

<211> 688

<212> DNA

<400> 11 gggaaaataacc cccccactag attgaaacccg cccgttcaaa atccatccat ccatcagccc
caacaccaat aaccgacgct gcaagaatgg cttctgcctt tccccatctc ctcctactca
ccaccctggc agctatctgt cttttctccg acgtcccttc cgccggcttg ggtggtcgcc
ccaaagatgc cttagtcggc gggtggagta aggctgacccc caaggaccca gaggtgctag
agaacggaaa atttgcata gatgagcaca acaaggaggc cggtaccaag ttggagttt
aaactgttgtt ggagggcgtag aagcaagtgg tggccggcac aaattacaag attgtataa
aggcatttggc tggcactgct tcaaattctgt acgaggccat tggtttggtc aagccctggc
tcaaattcaa gaagcttact tccttcagga aacttccctg atcagattt aaaaaatgtt
ataagcatgt gcatttcttg cttaaaaactg tggcatgaga ggtgtatgtt taatcatctg
tatttcttgc ttaaaaactgt ggtatgacta tgagagatgt ttgaagtgtt ctgtactaca
agagctttca tacatatgca agagttgaag cacttgggg cttctgtataa taataataat
acatcggtttt aaaaaaaaaa aaaaaaaaaa 688

<210> 12

<211> 124

<212> PRT

<213> Coffea canephora

SEQUENCE.TXT

<400> 12

Met Ala Ser Ala Phe Pro His Leu Leu Leu Leu Thr Thr Thr Leu Ala Ala
1 5 10 15

Ile Cys Leu Phe Ser Asp Val Pro Ser Ala Ala Leu Gly Gly Arg Pro
20 25 30

Lys Asp Ala Leu Val Gly Gly Trp Ser Lys Ala Asp Pro Lys Asp Pro
35 40 45

Glu Val Leu Glu Asn Gly Lys Phe Ala Ile Asp Glu His Asn Lys Glu
50 55 60

Ala Gly Thr Lys Leu Glu Phe Lys Thr Val Val Glu Ala Gln Lys Gln
65 70 75 80

Val Val Ala Gly Thr Asn Tyr Lys Ile Val Ile Lys Ala Leu Asp Gly
85 90 95

Thr Ala Ser Asn Leu Tyr Glu Ala Ile Val Trp Val Lys Pro Trp Leu
100 105 110

Lys Phe Lys Lys Leu Thr Ser Phe Arg Lys Leu Pro
115 120

<210> 13

<211> 697

<212> DNA

<213> Coffea canephora

<400> 13 gtttcgata gtcacaagca attgcaaaaa tctacttcgt acttataagc tagctagttc 60
ctcaaggaaa aaatggctac ggtcgcagcc aaatctgcta ctgccgctat tggtgctgga 120
cagaaaaaca tggtggtgg tggtctaagc tctactgttc ctccctcgatc gtcaaccgtc 180
aacccgaaag accctcacgt gattcagatc gcacaatttg cagttgcaaa ctacaacgcg 240
aaggccggga ccactgtggt ttggctgaat gtggaatatg gcttctggtg gattgacgat 300
gacacttaact acatgcttgc cattaaaact caggatctta cgggcacaca ttgcgacgta 360
gcattggttc gtgaaatatc ggagagcaat ggtacttata gcctcaaatg gtacaatcat 420
aacaataagt gaccacgcac tactcttgat cagctgagga tcaatgactt taattatata 480

SEQUENCE.TXT

tagtgttat ggtgtggctt tcagttatg catggatgtat	gtactgctgt catgcatacg	540
tctccctacg gtggtaactag tacattgaag gtgcagttgt	accgataaaa atgcaccatt	600
aaataaaaaaa aaatcaccgt ttatgttga gtttgtattc	ctgtatgata aaggtgcagt	660
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<210> 14

<211> 119

<212> PRT

<213> Coffea canephora

<400> 14

Met Ala Thr Val Ala Ala Lys Ser Ala	Thr Ala Ala Ile Gly Ala Gly	15
5	10	

Gln Lys Asn Met Val Gly Gly	Leu Ser Ser Thr Val Pro Pro Arg	30
20	25	

Ser Ser Thr Val Asn Pro Lys Asp Pro His Val Ile Gln Ile Ala Gln	35	40	45
-----------------------------------------------------------------	----	----	----

Phe Ala Val Ala Asn Tyr Asn Ala Lys Ala Gly Thr Thr Val Val Trp	50	55	60
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Leu Asn Val Glu Tyr Gly Phe Trp Trp Ile Asp Asp Asp Thr Tyr Tyr	65	70	75	80
-----------------------------------------------------------------	----	----	----	----

Met Leu Ala Ile Lys Thr Gln Asp Leu Thr Gly Thr His Cys Asp Val	85	90	95
-----------------------------------------------------------------	----	----	----

Ala Leu Val Arg Glu Ile Ser Glu Ser Asn Gly Thr Tyr Ser Leu Lys	100	105	110
-----------------------------------------------------------------	-----	-----	-----

Trp Tyr Asn His Asn Asn Lys
115

<210> 15

<211> 1367

<212> DNA

<213> Coffea canephora

SEQUENCE.TXT

<400> 15 ggcttacatc ttaaatccctg attttatag attcccttt cgtgaagttc aatcttcgca 60
gtcgctact aacatttggt agacatactt cgattatgaa aatggggaaag gctttccctt 120
ttgccgttgt attggctgtg atcttagtgg cggctatgag catggagatc acagaaagag 180
atttggcttc tgaggaaagc ttgtggact tgtacgaaag atggaggagc catcatactg 240
tttctcgaga ccttctgag aaacgaaagc gctttaatgt tttcaaggca aatgtccatc 300
acattcacaa ggtgaaccag aaggacaagc cttacaagct gaaactcaac agtttcgctg 360
atatgaccaa ccacgagttc agggattct acagttctaa ggtgaaacat taccggatgc 420
tccacggcag tcgtgctaat actggattta tgcatggaa gactgaaagt ttgccagcct 480
ccgttggattt gagaaagcaa ggagccgtga ctggcgtcaa gaatcaaggc aaatgtggta 540
gctgttggc atttcaact gtgggtggag tcgagggaaat caacaaaatc aaaacaggcc 600
aattagtttc tctgtccgag caagaacttg ttgactgtga aacggacaat gaaggatgca 660
acggaggact catggaaaat gcatacgagt ttattaagaa aagtggggaa ataacaactg 720
agaggctata tccctacaag gcaagagatg gcagctgtga ttcgtcaaag atgaatgccc 780
ctgctgtgac tattgatggg catgaaatgg taccgc当地 cgatgagaat gccttgatga 840
aagctgtgc taaccagcct gtatcgttag ctatagatgc gtctggctct gacatgcaat 900
tttattcaga ggggtgtatac gctggagact cgtgtggcaa tgagcttgat catggcgtgg 960
cggtcgtcgg ctacggact gctcttgacg gtactaaata ctggatagtg aagaactcat 1020
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aaggcggagt ttgtggata gcaatggagg cctccttatcc acttAAATTG tcctcccaca 1140
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tatatatata tttcagttaga ttcattgaat ttttagttaca gactacgcgc ttctgaagac 1260
tttagatcatc tcttaggcata gatTTATGTA atcctgctcc tgtgtatggtt tgaataaaaca 1320
ataagttagta ctaataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1367

<210> 16

<211> 359

<212> PRT

<213> Coffea canephora

<400> 16

Met Lys Met Gly Lys Ala Phe Leu Phe Ala Val Val Leu Ala Val Ile
1 5 10 15

22/23

SEQUENCE.TXT

Leu Val Ala Ala Met Ser Met Glu Ile Thr Glu Arg Asp Leu Ala Ser
20 25 30

Glu Glu Ser Leu Trp Asp Leu Tyr Glu Arg Trp Arg Ser His His Thr
35 40 45

Val Ser Arg Asp Leu Ser Glu Lys Arg Lys Arg Phe Asn Val Phe Lys
50 55 60

Ala Asn Val His His Ile His Lys Val Asn Gln Lys Asp Lys Pro Tyr
65 70 75 80

Lys Leu Lys Leu Asn Ser Phe Ala Asp Met Thr Asn His Glu Phe Arg
85 90 95

Glu Phe Tyr Ser Ser Lys Val Lys His Tyr Arg Met Leu His Gly Ser
100 105 110

Arg Ala Asn Thr Gly Phe Met His Gly Lys Thr Glu Ser Leu Pro Ala
115 120 125

Ser Val Asp Trp Arg Lys Gln Gly Ala Val Thr Gly Val Lys Asn Gln
130 135 140

Gly Lys Cys Gly Ser Cys Trp Ala Phe Ser Thr Val Val Gly Val Glu
145 150 155 160

Gly Ile Asn Lys Ile Lys Thr Gly Gln Leu Val Ser Leu Ser Glu Gln
165 170 175

Glu Leu Val Asp Cys Glu Thr Asp Asn Glu Gly Cys Asn Gly Gly Leu
180 185 190

Met Glu Asn Ala Tyr Glu Phe Ile Lys Lys Ser Gly Gly Ile Thr Thr
195 200 205

Glu Arg Leu Tyr Pro Tyr Lys Ala Arg Asp Gly Ser Cys Asp Ser Ser
210 215 220

Lys Met Asn Ala Pro Ala Val Thr Ile Asp Gly His Glu Met Val Pro
225 230 235 240

Ala Asn Asp Glu Asn Ala Leu Met Lys Ala Val Ala Asn Gln Pro Val
245 250 255

Ser Val Ala Ile Asp Ala Ser Gly Ser Asp Met Gln Phe Tyr Ser Glu
260 265 270

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SEQUENCE.TXT

Gly Val Tyr Ala Gly Asp Ser Cys Gly Asn Glu Leu Asp His Gly Val
275 280 285

Ala Val Val Gly Tyr Gly Thr Ala Leu Asp Gly Thr Lys Tyr Trp Ile
290 295 300

Val Lys Asn Ser Trp Gly Thr Gly Trp Gly Glu Gln Gly Tyr Ile Arg
305 310 315 320

Met Gln Arg Gly Val Asp Ala Ala Glu Gly Gly Val Cys Gly Ile Ala
325 330 335

Met Glu Ala Ser Tyr Pro Leu Lys Leu Ser Ser His Asn Pro Lys Pro
340 345 350

Ser Pro Pro Lys Asp Asp Leu
355